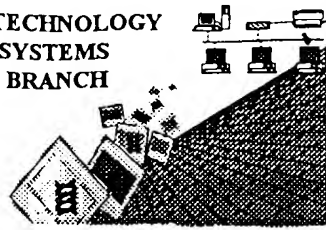


148E18, 1642

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/982,645
Source: 1600
Date Processed by STIC: 4/16/02

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APR 25 2002

TECH CENTER 1600/29

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 00000000

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

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APR 10 2002

TECH CENTER 1000 2900



1600

Does Not Comply
 Errors in Data Needed

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/982,645

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

3 <110> APPLICANT: CHEUNG, Nai-Kong V.
 5 <120> TITLE OF INVENTION: USES OF MONOCLONAL ANTIBODY 8H9
 7 <130> FILE REFERENCE: 638-B
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/982,645
 10 <141> CURRENT FILING DATE: 2002-03-08
 12 <150> PRIOR APPLICATION NUMBER: PCT/US01/32565
 13 <151> PRIOR FILING DATE: 2001-10-18
 15 <150> PRIOR APPLICATION NUMBER: 60/241,344
 16 <151> PRIOR FILING DATE: 2000-10-18
 18 <150> PRIOR APPLICATION NUMBER: 60/330,396
 19 <151> PRIOR FILING DATE: 2001-10-17
 21 <150> PRIOR APPLICATION NUMBER: 09/982,645
 22 <151> PRIOR FILING DATE: 2001-10-18
 24 <160> NUMBER OF SEQ ID NOS: 14
 26 <170> SOFTWARE: PatentIn version 3.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 731
 30 <212> TYPE: DNA
 31 <213> ORGANISM: 8H9scfv cDNA sequence
 33 <400> SEQUENCE: 1
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 36 tcctgcaagg ctcttggtca caccctcaca aactatgata taaactgggt gaggcagagg 120
 38 cctgaacagg gacttgagtg gattggatgg attttctctg gagatggtag tactcaatac 180
 40 aatgagaagt tcaagggcaa ggccacactg actacagaca catcctccag cacagcctac 240
 42 atgcagctca gcaggtgac atctgaggac tctgtgtctc atttctgtgc aagacagact 300
 44 acggctacct ggtttgctta ctggggccaa gggaccacgg tcaccgtctc ctcagatgga 360
 46 ggcggttcag gcggaggtgg ctctggcggt ggcggatcgg acatcgagct cactcagtct 420
 48 ccaaccaccc tgtctgtgac tccaggagat agagtctctc tttcctgcag ggccagccag 480
 50 agtattagcg actacttaca ctggtaccaa caaaaatcac atgagtctcc aaggcttctc 540
 52 atcaaatatg cttcccaatc catctctggg atcccccca ggttcagtgg cagtggatca 600
 54 gggtcagatt tcactctcag tatcaacagt gtggaacctg aagatgttgg agtgtattac 660
 56 tgtcaaaatg gtcacagctt tccgctcacg ttcgggtgctg ggaccaagct ggagctgaaa 720
 58 caggcggecg c 731
 61 <210> SEQ ID NO: 2
 62 <211> LENGTH: 243
 63 <212> TYPE: PRT
 64 <213> ORGANISM: 8H9scfv amino acid sequence
 66 <400> SEQUENCE: 2
 68 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 69 1 5 10 15
 72 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 73 20 25 30
 76 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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77          35          40          45
80 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
81      50          55          60
84 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Ser Thr Ala Tyr
85 65          70          75          80
88 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
89          85          90          95
92 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
93          100          105          110
96 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Ser
97      115          120          125
100 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
101      130          135          140
104 Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln
105 145          150          155          160
108 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
109          165          170          175
112 Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
113          180          185          190
116 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
117          195          200          205
120 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
121      210          215          220
124 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
125 225          230          235          240
128 Gln Ala Ala
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133 <211> LENGTH: 243
134 <212> TYPE: PRT
135 <213> ORGANISM: Mutated 8H9 scFv with decreased normal tissue adherence
137 <400> SEQUENCE: 3
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140 1          5          10          15
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144          20          25          30
147 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
148          35          40          45
151 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
152      50          55          60
155 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Ser Thr Ala Tyr
156 65          70          75          80
159 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
160          85          90          95
163 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
164          100          105          110
167 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser
168      115          120          125
171 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
172      130          135          140

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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176 145                      150                      155                      160
179 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
180                      165                      170                      175
183 Pro Gln Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
184                      180                      185                      190
187 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
188                      195                      200                      205
191 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
192      210                      215                      220
195 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Glu Leu Glu Leu Glu
196 225                      230                      235                      240
199 Gln Ala Ala
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204 <211> LENGTH: 22
205 <212> TYPE: DNA
206 <213> ORGANISM: [32P]r Probe
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213 <211> LENGTH: 21
214 <212> TYPE: DNA
215 <213> ORGANISM: Primer: ESBP1
217 <400> SEQUENCE: 5
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223 <212> TYPE: DNA
224 <213> ORGANISM: Primer: ESBP2
226 <400> SEQUENCE: 6
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232 <212> TYPE: DNA
233 <213> ORGANISM: Primer: EWS 696
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242 <213> ORGANISM: Primer: FLI 1 1041
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248 <210> SEQ ID NO: 9
249 <211> LENGTH: 25
250 <212> TYPE: DNA
251 <213> ORGANISM: Primer: G6PD1
253 <400> SEQUENCE: 9
254 ccggatcgac cactacctgg gcaag                                25

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:42

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\04162002\I982645.raw

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257 <210> SEQ ID NO: 10
258 <211> LENGTH: 26
259 <212> TYPE: DNA
260 <213> ORGANISM: Primer: G6PD2
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263 gttccccacg tactggccca ggacca
266 <210> SEQ ID NO: 11
267 <211> LENGTH: 24
268 <212> TYPE: DNA
269 <213> ORGANISM: Lightcycler Hybridization Probe: EWSHP1
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275 <210> SEQ ID NO: 12
276 <211> LENGTH: 18
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298 <400> SEQUENCE: 14
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/982,645

DATE: 04/16/2002

TIME: 14:31:43

Input Set : A:\638-B Sequence Project in PatentIn 3.1.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number